



Fig. S1. UPGMA tree (left panel) based on the copy numbers of 24 MIRU-VNTR loci (right panel, spoligotyping results whereby a repeat region's presence or absence is indicated by a black box or white box respectively) of the 16 strains investigated. The tree was calculated using the MIRU-VNTRplus server (www.miru-vnrplus.org; Distance Measure: Categorical).